

SEQUENCE LISTING

<110> Loughney, Kate
 <120> Phosphodiesterase 10
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 <140> 09/256,000
 <141> 1999-02-23
 <150> 60/075,508
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 <170> PatentIn Ver. 2.0

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 <222> (26)..(1423)

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aaa gtg aga cct gtg gcc atc aag caa ctc tcc gag aga gaa gaa tta 100
 Lys Val Arg Pro Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu
 10 15 20 25

atc cag agc gtg ctg gcg cag gtt gca gag cag ttc tca aga gca ttc 148
 Ile Gln Ser Val Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe
 30 35 40

aaa atc aat gaa ctg aaa gct gaa gtt gca aat cac ttg gct gtc cta 196
 Lys Ile Asn Glu Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu
 45 50 55

gag aaa cgc gtg gaa ttg gaa gga cta aaa gtg gtg gag att gag aaa 244
 Glu Lys Arg Val Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys
 60 65 70

tgc aag agt gac att aag aag atg agg gag gag ctg gcg gcc aga agc 292
 Cys Lys Ser Asp Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser
 75 80 85

agc agg acc aac tgc ccc tgt aag tac agt ttt ttg gat aac cac aag 340
 Ser Arg Thr Asn Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys
 90 95 100 105

aag ttg act cct cga cgc gat gtt ccc act tac ccc aag tac ctg ctc 388

Lys	Leu	Thr	Pro	Arg	Arg	Asp	Val	Pro	Thr	Tyr	Pro	Lys	Tyr	Leu	Leu		
			110				115					120					
tct	cca	gag	acc	atc	gag	gcc	ctg	cg	aag	ccg	acc	ttt	gac	gtc	tgg	436	
Ser	Pro	Glu	Thr	Ile	Glu	Ala	Leu	Arg	Lys	Pro	Thr	Phe	Asp	Val	Trp		
			125				130					135					
ctt	tgg	gag	ccc	aat	gag	atg	ctg	agc	tgc	ctg	gag	cac	atg	tac	cac	484	
Leu	Trp	Glu	Pro	Asn	Glu	Met	Leu	Ser	Cys	Leu	Glu	His	Met	Tyr	His		
	140						145				150						
gac	ctc	ggg	ctg	agg	gac	ttc	agc	atc	aac	cct	gtc	acc	ctc	agg		532	
Asp	Leu	Gly	Leu	Val	Arg	Asp	Phe	Ser	Ile	Asn	Pro	Val	Thr	Leu	Arg		
	155					160				165							
agg	tgg	ctg	ttc	tgc	gtc	cac	gac	aac	tac	aga	aac	aac	ccc	ttc	cac	580	
Arg	Trp	Leu	Phe	Cys	Val	His	Asp	Asn	Tyr	Arg	Asn	Asn	Pro	Phe	His		
	170			175			180			185							
aac	ttc	cg	cac	tgc	ttc	tgc	gtg	gcc	cag	atg	atg	tac	agc	atg	gtc	628	
Asn	Phe	Arg	His	Cys	Phe	Cys	Val	Ala	Gln	Met	Met	Tyr	Ser	Met	Val		
	190					195			200								
#tgg	ctc	tgc	agt	ctc	cag	gag	aag	ttc	tca	caa	acg	gat	atc	ctg	atc	676	
Trp	Leu	Cys	Ser	Leu	Gln	Glu	Lys	Phe	Ser	Gln	Thr	Asp	Ile	Leu	Ile		
	205				210				215								
cta	atg	aca	g	cc	atc	tgc	cac	gat	ctg	gac	cat	ccc	ggc	tac	aac	724	
Leu	Met	Thr	Ala	Ala	Ile	Cys	His	Asp	Leu	Asp	His	Pro	Gly	Tyr	Asn		
	220				225			230									
aac	acg	ta	c	ca	atc	ttc	g	cc	aca	g	atc	ttc	gg	cc	ta	at	772
Asn	Thr	Tyr	Gln	Ile	Asn	Ala	Arg	Thr	Glu	Leu	Ala	Val	Arg	Tyr	Asn		
	235				240			245									
gac	atc	tca	ccg	ctg	gag	aac	ca	ca	tgc	gg	gt	cc	ttc	ca	atc	820	
Asp	Ile	Ser	Pro	Leu	Glu	Asn	His	His	Cys	Ala	Val	Ala	Phe	Gln	Ile		
	250			255			260			265							
ctc	gcc	gag	cct	gag	tgc	aac	atc	ttc	tcc	aac	atc	cca	cct	gat	ggg	868	
Leu	Ala	Glu	Pro	Glu	Cys	Asn	Ile	Phe	Ser	Asn	Ile	Pro	Pro	Asp	Gly		
	270				275			280									
ttc	aag	cag	atc	cga	cag	gga	atg	atc	aca	tta	atc	ttg	gcc	act	gac	916	
Phe	Lys	Gln	Ile	Arg	Gln	Gly	Met	Ile	Thr	Leu	Ile	Leu	Ala	Thr	Asp		
	285			290				295									
atg	gca	aga	cat	gca	gaa	att	atg	gat	tct	ttc	aaa	gag	aaa	atg	gag	964	
Met	Ala	Arg	His	Ala	Glu	Ile	Met	Asp	Ser	Phe	Lys	Glu	Lys	Met	Glu		
	300				305				310								
aat	ttt	gac	ta	gc	a	ac	g	g	ca	at	cc	tt	gg	at	tt	1012	
Asn	Phe	Asp	Tyr	Ser	Asn	Glu	Glu	His	Met	Thr	Leu	Leu	Lys	Met	Ile		
	315				320			325									
ttg	ata	aaa	tgc	tgt	gat	atc	tct	aa	gag	gtc	cgt	cca	atg	gaa	gtc	1060	
Leu	Ile	Lys	Cys	Cys	Asp	Ile	Ser	Asn	Glu	Val	Arg	Pro	Met	Glu	Val		

330	335	340	345	
gca gag cct tgg gtg gac tgg tta tta gag gaa tat ttt atg cag agc Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser 350	355	360		1108
gac cgt gag aag tca gaa ggc ctt cct gtg gca ccg ttc atg gac cga Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg 365	370	375		1156
gac aaa gtg acc aag gcc aca gcc cag att ggg ttc atc aag ttt gtc Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val 380	385	390		1204
ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc ccc atg gtt gag Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu 395	400	405		1252
gag atc atg ctg cag cca ctt tgg gaa tcc cga gat cgc tac gag gag Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu 410	415	420	425	1300
ctg aag cgg ata gat gac gcc atg aaa gag tta cag aag aag act gac Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp 430	435	440		1348
agc ttg acg tct ggg gcc acc gag aag tcc aga ggg aga agc aga gat Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Gly Arg Ser Arg Asp 445	450	455		1396
tggtg aaa aac agt gaa gga gac tgg tggagaaagc gggggggcgtg Val Lys Asn Ser Glu Gly Asp Cys Ala 460	465			1443
ggctgcagttc tggacgggct ggccgagctg cgccggatcc ttgtgcaggg aagagctgcc ctgggcacct ggcaccacaa gaccatgttt tctaagaacc atttt				1503
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Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala 35 40 45				
Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu 50 55 60				

Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile Lys Lys
65 70 75 80

Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys Pro Cys
85 90 95

Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg Arg Asp
100 105 110

Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile Glu Ala
115 120 125

Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn Glu Met
130 135 140

Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp
145 150 155 160

Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His
165 170 175

Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys
180 185 190

Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu
195 200 205

Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys
210 215 220

His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala
225 230 235 240

Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn
245 250 255

His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn
260 265 270

Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly
275 280 285

Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile
290 295 300

Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu
305 310 315 320

Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile
325 330 335

Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys
340 345 350

Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly
355 360 365

Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr
370 375 380

Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr
385 390 395 400

Val Thr Lys Leu Phe Pro Met Val Glu Ile Met Leu Gln Pro Leu
405 410 415

Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala
420 425 430

Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr
435 440 445

Glu Lys Ser Arg Gly Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp
450 455 460

Cys Ala
465

<210> 3

<211> 225

<212> DNA

<213> Homo sapiens

<220>

<223> Nucleotides at positions 130, 186, and 205 are
either A, T, G, or C.

<400> 3

agcgaccgtg agaagtcaga aggccttcct gtggAACCGT tcataggaccg agacaaagt 60

accaggccca cagccagat tggttcatc aagtttgc 120

gtgaccaagn tcttcccat ggttggaggat atcatgctgc agccactttg ggaatcccga 180

gatcgntacg aggagctgaa gcggntagat gacgccatga aagag 225

<210> 4

<211> 158

<212> DNA

<213> Homo sapiens

<220>

<223> Nucleotides at positions 12, 36, 61, and 109 are
either A, T, G, or C.

<400> 4

gtaccagatc antgccccgca cagagctggc ggtccgntac aatgacatct caccgttg 60

gnaaccacca ctgcgccgtg gccttccaga tcctcgccga gcctgagtg 120

ccaacatccc acctgatggg ttcaaggcaga tccgacag 158

<210> 5
<211> 98
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 14, 22, and 50 are either A, T, C, or G.

<400> 5
gagaacacca ctgngccgtg gncttccaga tcctcgccga gcctgagtgn aacatcttct 60
ccaacatccc acctgatggg ttcaaggcaga tccgacag 98

<210> 6
<211> 418
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 1, 267, 352, 400, and 411 are either A, T, G, or C.

<400> 6
nggttaactg gcgcacatcttgc tctttctctg agaacagcga tctggttatg gggcatttct 60
gtctctaactg tcactgtctg ctgcattccc tgcagagcga ccgtgagaag tcagaaggcc 120
ttcccggtggc cccgttcatg gaccgagaca aagtgaccaa ggccacagcc caggattggg 180
tttcatcaag tttgtcctga tcccaatgtt tgaaacagtgc accaagctct tccccatggg 240
tgagggaga ttcatgctgg cagccanttt gggaaatccc gaggattcgc tacgagggag 300
tttgaagcgg gattaggatg gacggccatg gaaaggagtt ttacaggaag gnaggatttg 360
acagtttga agttttgggg gggccaccga ggaagttccn ggaggaggag naggcaga 418

<210> 7
<211> 428
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 1, 82, 92, 130, 347, 390, and 396 are either A, T, G, or C.

<400> 7
nagaaaaaaag tgaacaaaat gtttcttaga aaacatggtc ttgtggtgcc aggtgcccag 60
ggagctcttc cctgcacaag gntcccgccgc antcgccag cccgtccaga actgcagcca 120
cgccccccgn tttcctcagg cacagtctcc ttcactgttt ttcacatctc tgcttctctc 180
tctggacttc tcgggtggccc cagacgtcaa gctgtcagtc ttcttctgta actctttcat 240

ggcggtcatc tatccgcttc agtcctcggtt aggcgatctc ggggattccc aaagtgggct 300
gcagcatgat cttccctcaac catggggggg aggagcttgg ggcactngtt ttcaaaaatt 360
gggggatcag gggacaaaact ttgattggan cccatnttgg ggctttggg cctttgggc 420
aatttttg 428

<210> 8
<211> 438
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 63, 98, 107, 188, 203,
206, 238, 252, 297, 370, 389, and 427 are either
A, T, G, or C.

<400> 8
ttttttttt tttttttgt atcagtgaac aaaatggttc ttagaaaaca tggtcttgc 60
gttccagggtg cccagggagc tcttccctgc acaagganc cgcgcantcg gccagccgt 120
ccagaactgc agccacgccc cccgtttcc tcagggcacag tctccttcac tgttttcac 180
atctctgntt ctctctctgg ganttntcgg tgggccccag aacgtcaagc tgtcagtntt 240
cttctgttaac tnttcatgg gcgtcatcta tccgtttcag cttccctcgta ggcgtatntt 300
gggattccca aagtgggctg gcagcatgga tcttcctcaa accatgggg gaaggagttt 360
gggtcaattn tttcaaaaac attggggnt cagggacaaa atttgtatgg aaacccaatt 420
tgggggntgt gggccttg 438

<210> 9
<211> 262
<212> DNA
<213> Mus musculus

<400> 9
gagaattttt actacagcaa cgaggagcac ctgaccctgc tgaagatgat tctcataaaa 60
tgctgtata tctccaatga agtccgtccc atggaggtgg cagaatcgtg ggtggactgt 120
ttactggaag aatattttat gcagagtgcac cgtgagaagt ccgaagcctt cctgtggccc 180
cattcatgga ccgagacaaa gtgaccaaag caacagccca aattgggttc atcaagttt 240
tcctgatccc aatgtttgaa ac 262

<210> 10
<211> 250
<212> DNA

<213> Mus musculus

<400> 10
gagaattttg actacagcaa cgaggagcac ctgaccctgc tgaagatgat tctcataaaa 60
tgctgtgata tctccaatga agtccgtccc atggaggtgg cagaatcgtg ggtggactgt 120
ttactggaag aatattttat gcagagtgc acgtgagaagt ccgaagcctt cctgtggccc 180
attcatggac cgagacaaag tgaccaaagc aacagccaaa ttgggttcat caagtttgc 240
tgtccaatgt 250

<210> 11

<211> 459
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotides at positions 155, 393, and 442 are
either A, T, G, or C.

<400> 11
Gataatcttg gccactgaca tggcaagaca tgcagaaatt atggatttt tcaaagagaa 60
aaatggagaat tttgactaca gcaacgagga gcacatgacc ctggtagtg gcttattctg 120
cctgggtgg cagccaggcg gttggctgg cgaanaggtt catccatcca gtcacactg 180
gaagccaaga agctgaaatt attagtcttc ttggacaag gtgtctataa atctggttt 240
caaggtcatg actcttacta ggaaagtccg ggcagggcct ccctcctgat gggcctcct 300
tcatggtcag aggcagcatt ctccattcc tccatctctt ttgggatttt gaaggagata 360
aagtgggtg aaggccgtgc attctcgctc tgnntttcca gagaattaaa accagtttc 420
ccttgaaggc acagccccag cttggcattt tgaaagttg 459

<210> 12

<211> 599
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (99)..(443)

<400> 12
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agaacagcga tctggttatg gggcatttct gtctctaa tgt cac tgt ctg ctg cat 116
Cys His Cys Leu Leu His
1 5

tcc ctg cag agc gac cgt gag aag tca gaa ggc ctt ccc gtg gcc ccg Ser Leu Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro 10 15 20	164	
ttc atg gac cga gac aaa gtg acc aag gcc aca gcc cag att ggg ttc Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe 25 30 35	212	
atc aag ttt gtc ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe 40 45 50	260	
ccc atg gtt gag gag atc atg ctg cag cca ctt tgg gaa tcc cga gat Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp 55 60 65 70	308	
cgc tac gag gag ctg aag cgg ata gat gac gcc atg aaa gag tta cag Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln 75 80 85	356	
aag aag act gac agc ttg acg tct ggg gcc acc gag aag tcc aga gag Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu 90 95 100	404	
aga agc aga gat gtg aaa aac agt gaa gga gac tgt gcc tgagggaaagc Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala 105 110 115	453	
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ctgataaaaa aaaaaaaaaa aaaaaaa 599		
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Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala 20 25 30		
Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu 35 40 45		
Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro 50 55 60		
Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp 65 70 75 80		
Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala		

85

90

95

Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu Gly
100 105 110

Asp Cys Ala
115

<210> 14
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 14
agtgcattt accgtgagaa gtcagaag 28

<210> 15
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 15
gtcaaaatc acatggctt gtggtgcc 28

<210> 16
<211> 1303
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (107)..(1066)

<400> 16
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cttactaacg ttagccccca gcctagctat ggagggtgca tgctga gcc ctg gag 115
Ala Leu Glu
1

cac atg tac cac gac ctc ggg ctg gtc agg gac ttc agc atc aac cct 163
His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro
5 10 15

gtc acc ctc agg agg tgg ctg ttc tgc gtc cac gac aac tac aga aac 211
Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn
20 25 30 35

aac ccc ttc cac aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met 40 45 50	259
tac agc atg gtc tgg ctc tgc agt ctc cag gag aag ttc tca caa acg Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr 55 60 65	307
gat atc ctg atc cta atg aca gcg gcc atc tgc cac gat ctg gac cat Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His 70 75 80	355
ccc ggc tac aac aac acg tac cag atc aat gcc cgc aca gag ctg gcg Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala 85 90 95	403
gtc cgc tac aat gac atc tca ccg ctg gag aac cac cac tgc gcc gtg Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His His Cys Ala Val 100 105 110 115	451
gcc ttc cag atc ctc gcc gag cct gag tgc aac atc ttc tcc aac atc Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile 120 125 130	499
cca cct gat ggg ttc aag cag atc cga cag gga atg atc aca tta atc Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met Ile Thr Leu Ile 135 140 145	547
ttg gcc act gac atg gca aga cat gca gaa att atg gat tct ttc aaa Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met Asp Ser Phe Lys 150 155 160	595
gag aaa atg gag aat ttt gac tac agc aac gag gag cac atg acc ctg Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu His Met Thr Leu 165 170 175	643
ctg aag atg att ttg ata aaa tgc tgt gat atc tct aac gag gtc cgt Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser Asn Glu Val Arg 180 185 190 195	691
cca atg gaa gtc gca gag cct tgg gtg gac tgt tta tta gag gaa tat Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr 200 205 210	739
ttt atg cag agc gac cgt gag aag tca gaa ggc ctt cct gtg gca ccg Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro 215 220 225	787
ttc atg gac cga gac aaa gtg acc aag gcc aca gcc cag att ggg ttc Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe 230 235 240	835
atc aag ttt gtc ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe 245 250 255	883
ccc atg gtt gag gag atc atg ctg cag cca ctt tgg gaa tcc cga gat	931

Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp	260	265	270	275	
cgc tac gag gag ctg aag cgg ata gat gac gcc atg aaa gag tta cag					979
Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln	280		285	290	
aag aag act gac agc ttg acg tct ggg gcc acc gag aag tcc aga gag					1027
Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu	295	300		305	
aga agc aga gat gtg aaa aac agt gaa gga gac tgt gcc tgagggaaagc					1076
Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala	310	315		320	
ggggggcggtg gctgcgttc tggacgggct ggccgagctg cgcgggatcc ttgtcaggg					1136
aagagctgcc ctgggcacct ggcaccacaa gaccatgttt tctaaagaacc attttgttca					1196
ctgatacataaa aaaaaaaaaaag gaattcatga tgctgtacag aattttatattt ttaaaactgtc					1256
ttttaaataaa tatattctta tacggaaaaa aaaaaaaaaa aaaaaaaaaa					1303
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Ala Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe Ser					
1	5	10	15		
 Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp Asn					
20	25	30			
 Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val Ala					
35	40	45			
 Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys Phe					
50	55	60			
 Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His Asp					
65	70	75	80		
 Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg Thr					
85	90	95			
 Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His His					
100	105	110			
 Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile Phe					
115	120	125			
 Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met Ile					
130	135	140			

Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met Asp
145 150 155 160

Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu His
165 170 175

Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser Asn
180 185 190

Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu Leu
195 200 205

Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro
210 215 220

Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln
225 230 235 240

Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr
245 250 255

Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu
260 265 270

Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys
275 280 285

Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys
290 295 300

Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala
305 310 315 320

<210> 18

<211> 1887

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (74)..(1672)

<400> 18

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cgccggggcgc agg atg gga tcc ggc tcc agc tac cgg ccc aag gcc 109
Met Gly Ser Gly Ser Ser Tyr Arg Pro Lys Ala
1 5 10

atc tac ctg gac atc gat gga cgc att cag aag gta atc ttc agc aag 157
Ile Tyr Leu Asp Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys
15 20 25

tac tgc aac tcc agc gac atc atg gac ctg ttc tgc atc gcc acc ggc 205
Tyr Cys Asn Ser Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly
30 35 40

ctg cct cgg aac acg acc atc tcc ctg ctg acc acc gac gac gcc atg Leu Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met 45 50 55 60	253
gtc tcc atc gac ccc acc atg ccc gcg aat tca gaa cgc act ccg tac Val Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr 65 70 75	301
aaa gtg aga cct gtg gcc atc aag caa ctc tcc gag aga gaa gaa tta Lys Val Arg Pro Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu 80 85 90	349
atc cag agc gtg ctg gcg cag gtt gca gag cag ttc tca aga gca ttc Ile Gln Ser Val Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe 95 100 105	397
aaa atc aat gaa ctg aaa gct gaa gtt gca aat cac ttg gct gtc cta Lys Ile Asn Glu Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu 110 115 120	445
gag aaa cgc gtg gaa ttg gaa gga cta aaa gtg gtg gag att gag aaa Glu Lys Arg Val Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys 125 130 135 140	493
tgc aag agt gac att aag aag atg agg gag gag ctg gcg gcc aga agc Cys Lys Ser Asp Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser 145 150 155	541
agc agg acc aac tgc ccc tgt aag tac agt ttt ttg gat aac cac aag Ser Arg Thr Asn Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys 160 165 170	589
aag ttg act cct cga cgc gat gtt ccc act tac ccc aag tac ctg ctc Lys Leu Thr Pro Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu 175 180 185	637
tct cca gag acc atc gag gcc ctg cgg aag ccg acc ttt gac gtc tgg Ser Pro Glu Thr Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp 190 195 200	685
ctt tgg gag ccc aat gag atg ctg agc tgc ctg gag cac atg tac cac Leu Trp Glu Pro Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His 205 210 215 220	733
gac ctc ggg ctg gtc agg gac ttc agc atc aac cct gtc acc ctc agg Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg 225 230 235	781
agg tgg ctg ttc tgc gtc cac gac aac tac aga aac aac ccc ttc cac Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His 240 245 250	829
aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg tac agc atg gtc Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val 255 260 265	877
tgg ctc tgc agt ctc cag gag aag ttc tca caa acg gat atc ctg atc	925

Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile			
270	275	280	
ct a atg aca gca gcc atc tgc cac gat ctg gac cat ccc ggc tac aac			973
Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn			
285	290	295	300
aac acg tac cag atc aat gcc cgc aca gag ctg gcg gtc cgc tac aat			1021
Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn			
305	310	315	
gac atc tca ccg ctg gag aac cac cac tgc gcc gtg gcc ctc cag atc			1069
Asp Ile Ser Pro Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile			
320	325	330	
ctc gcc gag cct gag tgc aac atc ttc tcc aac atc cca cct gat ggg			1117
Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly			
335	340	345	
ttc aag cag atc cga cag gga atg atc aca tta atc ttg gcc act gac			1165
Phe Lys Gln Ile Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp			
350	355	360	
atg gca aga cat gca gaa att atg gat tct ttc aaa gag aaa atg gag			1213
Met Ala Arg His Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu			
365	370	375	380
aat ttt gac tac agc aac gag gag cac atg acc ctg ctg aag atg att			1261
Asn Phe Asp Tyr Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile			
385	390	395	
ttg ata aaa tgc tgt gat atc tct aac gag gtc cgt cca atg gaa gtc			1309
Leu Ile Lys Cys Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val			
400	405	410	
gca gag cct tgg gtc gac tgt tta tta gag gaa tat ttt atg cag agc			1357
Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser			
415	420	425	
gac cgt gag aag tca gaa ggc ctt cct gtc gca ccg ttc atg gac cga			1405
Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg			
430	435	440	
gac aaa gtg acc aag gcc aca gcc cag att ggg ttc atc aag ttt gtc			1453
Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val			
445	450	455	460
ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc ccc atg gtt gag			1501
Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu			
465	470	475	
gag atc atg ctg cag cca ctt tgg gaa tcc cga gat cgc tac gag gag			1549
Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu			
480	485	490	
ctg aag cgg ata gat gac gcc atg aaa gag tta cag aag aag act gac			1597
Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln Lys Thr Asp			

495

500

505

agc ttg acg tct ggg gcc acc gag aag tcc aga gag aga agc aga gat 1645
 Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp
 510 515 520

gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc ggggggcgtg 1692
 Val Lys Asn Ser Glu Gly Asp Cys Ala
 525 530

gctgcagttc tggacgggct ggccgagctg cgcggatcc ttgtgcaggg aagagctgcc 1752
 ctgggcacct ggcaccacaa gaccatgttt tctaagaacc attttggtca ctgataaaaa 1812
 aaaaaaaaaa ggaattcatg atgctgtaca gaattttatt tttaaactgt ctttaaata 1872
 atatattctt atacg 1887

<210> 19
 <211> 533
 <212> PRT
 <213> Homo sapiens

<400> 19
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Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser
 20 25 30

Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn
 35 40 45

Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp
 50 55 60

Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro
 65 70 75 80

Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val
 85 90 95

Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu
 100 105 110

Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val
 115 120 125

Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp
 130 135 140

Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn
 145 150 155 160

Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro
 165 170 175

Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr
 180 185 190
 Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro
 195 200 205
 Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu
 210 215 220
 Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe
 225 230 235 240
 Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His
 245 250 255
 Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser
 260 265 270
 Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala
 275 280 285
 Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln
 290 295 300
 Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro
 305 310 315 320
 Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro
 325 330 335
 Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile
 340 345 350
 Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His
 355 360 365
 Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr
 370 375 380
 Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys
 385 390 395 400
 Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp
 405 410 415
 Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys
 420 425 430
 Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr
 435 440 445
 Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met
 450 455 460
 Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu
 465 470 475 480

Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile
485 490 495

Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser
500 505 510

Gly Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser
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Glu Gly Asp Cys Ala
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<210> 20

<211> 1967

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2)..(1741)

<400> 20

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Tyr Leu Asp Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr
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tgc aac tcc agc gac atc atg gac ctg ttc tgc atc gcc acc ggc ctg 97
Cys Asn Ser Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu
20 25 30

cct cgg aac acg acc atc tcc ctg ctg acc acc gac gac gcc atg gtc 145
Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val
35 40 45

tcc atc gac ccc acc atg ccc gcg aat tca gaa cgc act ccg tac aaa 193
Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys
50 55 60

gtg aga cct gtg gcc atc aag caa ctc tcc gct gat gtc gag gac aag 241
Val Arg Pro Val Ala Ile Lys Gln Leu Ser Ala Asp Val Glu Asp Lys
65 70 75 80

aga acc aca agc cgt ggc cag tct gct gag aga cca ctg agg gac aga 289
Arg Thr Thr Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg
85 90 95

cgg gtt gtg ggc ctg gag cag ccc cgg agg gaa gga gca ttt gaa agt 337
Arg Val Val Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser
100 105 110

gga cag gta gag ccc agg ccc aga gag ccc cag ggc tgc tac cag gaa 385
Gly Gln Val Glu Pro Arg Pro Arg Glu Pro Gln Gly Cys Tyr Gln Glu
115 120 125

ggc cag cgc atc cct cca gag aga gaa gaa tta atc cag agc gtg ctg 433
Gly Gln Arg Ile Pro Pro Glu Arg Glu Glu Leu Ile Gln Ser Val Leu

130

135

140

gcg cag gtt gca gag cag ttc tca aga gca ttc aaa atc aat gaa ctg Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu 145 150 155 160	481
aaa gct gaa gtt gca aat cac ttg gct gtc cta gag aaa cgc gtg gaa Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu 165 170 175	529
ttg gaa gga cta aaa gtg gtg gag att gag aaa tgc aag agt gac att Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile 180 185 190	577
aag aag atg agg gag gag ctg gcg gcc aga agc agc agg acc aac tgc Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys 195 200 205	625
ccc tgt aag tac agt ttt ttg gat aac cac aag aag ttg act cct cga Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg 210 215 220	673
cgc gat gtt ccc act tac ccc aag tac ctg ctc tct cca gag acc atc Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile 225 230 235 240	721
gag gcc ctg cgg aag ccg acc ttt gac gtc tgg ctt tgg gag ccc aat Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn 245 250 255	769
gag atg ctg agc tgc ctg gag cac atg tac cac gac ctc ggg ctg gtc Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val 260 265 270	817
agg gac ttc agc atc aac cct gtc acc ctc agg agg tgg ctg ttc tgc Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys 275 280 285	865
gtc cac gac aac tac aga aac aac ccc ttc cac aac ttc cgg cac tgc Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys 290 295 300	913
ttc tgc gtg gcc cag atg atg tac agc atg gtc tgg ctc tgc agt ctc Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu 305 310 315 320	961
cag gag aag ttc tca caa acg gat atc ctg atc cta atg aca gcg gcc Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala 325 330 335	1009
atc tgc cac gat ctg gac cat ccc ggc tac aac aac acg tac cag atc Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile 340 345 350	1057
aat gcc cgc aca gag ctg gcg gtc cgc tac aat gac atc tca ccg ctg Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu 355 360 365	1105

gag aac cac cac tgc gcc gtg gcc ttc cag atc ctc gcc gag cct gag	1153
Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu	
370 375 380	
tgc aac atc ttc tcc aac atc cca cct gat ggg ttc aag cag atc cga	1201
Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg	
385 390 395 400	
cag gga atg atc aca tta atc ttg gcc act gac atg gca aga cat gca	1249
Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala	
405 410 415	
gaa att atg gat tct ttc aaa gag aaa atg gag aat ttt gac tac agc	1297
Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser	
420 425 430	
aac gag gag cac atg acc ctg ctg aag atg att ttg ata aaa tgc tgt	1345
Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys	
435 440 445	
gat atc tct aac gag gtc cgt cca atg gaa gtc gca gag cct tgg gtg	1393
Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val	
450 455 460	
gac tgt tta tta gag gaa tat ttt atg cag agc gac cgt gag aag tca	1441
Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser	
465 470 475 480	
gaa ggc ctt cct gtg gca ccg ttc atg gac cga gac aaa gtg acc aag	1489
Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys	
485 490 495	
gcc aca gcc cag att ggg ttc atc aag ttt gtc ctg atc cca atg ttt	1537
Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe	
500 505 510	
gaa aca gtg acc aag ctc ttc ccc atg gtt gag gag atc atg ctg cag	1585
Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln	
515 520 525	
cca ctt tgg gaa tcc cga gat cgc tac gag gag ctg aag cgg ata gat	1633
Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp	
530 535 540	
gac gcc atg aaa gag tta cag aag aag act gac agc ttg acg tct ggg	1681
Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly	
545 550 555 560	
gcc acc gag aag tcc aga gag aga agc aga gat gtg aaa aac agt gaa	1729
Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu	
565 570 575	
gga gac tgt gcc tgaggaaaagc gggggcgctg gctgcagttc tggacgggct	1781
Gly Asp Cys Ala	
580	
ggcccgagctg cgccggatcc ttgtgcaggg aagagctgcc ctggccaccc ggcaccacaa	1841

gaccatgttt tctaagaacc attttggta ctgatacaaa aaaaaaaaaa ggaattcatg 1901
atgctgtaca gaattttatt tttaaactgt cttttaata atatattctt atacggaaaa 1961
aaaaaaaaa 1967

<210> 21
<211> 580
<212> PRT
<213> Homo sapiens

<400> 21
Tyr Leu Asp Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr
1 5 10 15

Cys Asn Ser Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu
20 25 30

Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val
35 40 45

Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys
50 55 60

Val Arg Pro Val Ala Ile Lys Gln Leu Ser Ala Asp Val Glu Asp Lys
65 70 75 80

Arg Thr Thr Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg
85 90 95

Arg Val Val Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser
100 105 110

Gly Gln Val Glu Pro Arg Pro Arg Glu Pro Gln Gly Cys Tyr Gln Glu
115 120 125

Gly Gln Arg Ile Pro Pro Glu Arg Glu Glu Leu Ile Gln Ser Val Leu
130 135 140

Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu
145 150 155 160

Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu
165 170 175

Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile
180 185 190

Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys
195 200 205

Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg
210 215 220

Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile
225 230 235 240

Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn
 245 250 255
 Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val
 260 265 270
 Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys
 275 280 285
 Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys
 290 295 300
 Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu
 305 310 315 320
 Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala
 325 330 335
 Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile
 340 345 350
 Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu
 355 360 365
 Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu
 370 375 380
 Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg
 385 390 395 400
 Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala
 405 410 415
 Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser
 420 425 430
 Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys
 435 440 445
 Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val
 450 455 460
 Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser
 465 470 475 480
 Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys
 485 490 495
 Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe
 500 505 510
 Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln
 515 520 525
 Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp
 530 535 540

Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly
545 550 555 560

Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu
565 570 575

Gly Asp Cys Ala
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<211> 1457
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (164)..(1453)

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ggaaagtaca gtaaaaagtc cgagtgcage cgccgggcgc agg atg gga tcc ggc 175
Met Gly Ser Gly
1
tcc tcc agc tac cgg ccc aag gcc atc tac ctg gac atc gat gga cgc 223
Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp Ile Asp Gly Arg
5 10 15 20
att cag aag gta atc ttc agc aag tac tgc aac tcc agc gac atc atg 271
Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser Ser Asp Ile Met
25 30 35
gac ctg ttc tgc atc gcc acc ggc ctg cct cgg aac acg acc atc tcc 319
Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn Thr Thr Ile Ser
40 45 50
ctg ctg acc acc gac gac gcc atg gtc tcc atc gac ccc acc atg ccc 367
Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp Pro Thr Met Pro
55 60 65
gcg aat tca gaa cgc act ccg tac aaa gtg aga cct gtg gcc atc aag 415
Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro Val Ala Ile Lys
70 75 80
caa ctc tcc gag aga gaa gaa tta atc cag agc gtg ctg gcg cag gtt 463
Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val Leu Ala Gln Val
85 90 95 100
gca gag cag ttc tca aga gca ttc aaa atc aat gaa ctg aaa gct gaa 511
Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala Glu
105 110 115
gtt gca aat cac ttg gct gtc cta gag aaa cgc gtg gaa ttg gaa gga 559

Val	Ala	Asn	His	Leu	Ala	Val	Leu	Glu	Lys	Arg	Val	Glu	Leu	Glu	Gly	
120						125					130					
ct a	aaa	gtg	gtg	gag	att	gag	aaa	tgc	aag	agt	gac	att	aag	aag	atg	607
Leu	Lys	Val	Val	Glu	Ile	Glu	Lys	Cys	Lys	Ser	Asp	Ile	Lys	Lys	Met	
135						140					145					
agg	gag	gag	ctg	gcf	gcc	aga	agc	agc	agg	acc	aac	tgc	ccc	tgt	aag	655
Arg	Glu	Glu	Leu	Ala	Ala	Arg	Ser	Ser	Arg	Thr	Asn	Cys	Pro	Cys	Lys	
150						155					160					
tac	agt	ttt	ttg	gat	aac	cac	aag	aag	ttg	act	cct	cga	cgc	gat	gtt	703
Tyr	Ser	Phe	Leu	Asp	Asn	His	Lys	Lys	Leu	Thr	Pro	Arg	Arg	Asp	Val	
165						170				175				180		
ccc	act	tac	ccc	aag	tac	ctg	ctc	tct	cca	gag	acc	atc	gag	gcc	ctg	751
Pro	Thr	Tyr	Pro	Lys	Tyr	Leu	Leu	Ser	Pro	Glu	Thr	Ile	Glu	Ala	Leu	
185						190				195						
cg g	aag	ccg	acc	ttt	gac	gtc	tgg	ctt	tgg	gag	ccc	aat	gag	atg	ctg	799
Arg	Lys	Pro	Thr	Phe	Asp	Val	Trp	Leu	Trp	Glu	Pro	Asn	Glu	Met	Leu	
200						205				210						
agc	tgc	ctg	gag	cac	atg	tac	cac	gac	ctc	ggg	ctg	gtc	agg	gac	ttc	847
Ser	Cys	Leu	Glu	His	Met	Tyr	His	Asp	Leu	Gly	Leu	Val	Arg	Asp	Phe	
215						220				225						
agc	atc	aac	cct	gtc	acc	ctc	agg	agg	tgg	ctg	ttc	tgc	gtc	cac	gac	895
Ser	Ile	Asn	Pro	Val	Thr	Leu	Arg	Arg	Trp	Leu	Phe	Cys	Val	His	Asp	
230						235				240						
aac	tac	aga	aac	aac	ccc	ttc	cac	aac	ttc	cg g	cac	tgc	ttc	tgc	gtg	943
Asn	Tyr	Arg	Asn	Asn	Pro	Phe	His	Asn	Phe	Arg	His	Cys	Phe	Cys	Val	
245						250				255				260		
gcc	cag	atg	atg	tac	agc	atg	gtc	tgg	ctc	tgc	agt	ctc	cag	gag	aag	991
Ala	Gln	Met	Met	Tyr	Ser	Met	Val	Trp	Leu	Cys	Ser	Leu	Gln	Glu	Lys	
265						270				275						
ttc	tca	caa	acg	gat	atc	ctg	atc	cta	atg	aca	gcf	gcc	atc	tgc	cac	1039
Phe	Ser	Gln	Thr	Asp	Ile	Leu	Ile	Leu	Met	Thr	Ala	Ala	Ile	Cys	His	
280						285				290						
gat	ctg	gac	cat	ccc	ggc	tac	aac	aac	acg	tac	cag	atc	aat	gcc	cgc	1087
Asp	Leu	Asp	His	Pro	Gly	Tyr	Asn	Asn	Thr	Tyr	Gln	Ile	Asn	Ala	Arg	
295						300				305						
aca	gag	ctg	gcf	gtc	cgc	tac	aat	gac	atc	tca	ccg	ctg	gag	aac	cac	1135
Thr	Glu	Ileu	Ala	Val	Arg	Tyr	Asn	Asp	Ile	Ser	Pro	Leu	Glu	Asn	His	
310						315				320						
cac	tgc	gcc	gtg	gcc	ttc	cag	atc	ctc	gcc	gag	cct	gag	tgc	aac	atc	1183
His	Cys	Ala	Val	Ala	Phe	Gln	Ile	Leu	Ala	Glu	Pro	Glu	Cys	Asn	Ile	
325						330				335				340		
ttc	tcc	aac	atc	cca	cct	gat	ggg	ttc	aag	cag	atc	cga	cag	gga	atg	1231
Phe	Ser	Asn	Ile	Pro	Pro	Asp	Gly	Phe	Lys	Gln	Ile	Arg	Gln	Gly	Met	

345

350

355

atc aca tta atc ttg gcc act gac atg gca aga cat gca gaa att atg 1279
 Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met
 360 365 370

gat tct ttc aaa gag aaa atg gag aat ttt gac tac agc aac gag gag 1327
 Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu
 375 380 385

cac atg acc ctg ctg aag atg att ttg ata aaa tgc tgt gat atc tct 1375
 His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser
 390 395 400

aac gag gtc cgt cca atg gaa gtc gca gag cct tgg gtg gac tgt tta 1423
 Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu
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tta gag gaa tat ttt atg cag agc gac cgt gaga 1457
 Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg
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Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser
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Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn
 35 40 45

Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp
 50 55 60

Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro
 65 70 75 80

Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val
 85 90 95

Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu
 100 105 110

Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val
 115 120 125

Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp
 130 135 140

Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn

145 150 155 160
Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro
165 170 175
Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr
180 185 190
Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro
195 200 205
Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu
210 215 220
Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe
225 230 235 240
Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His
245 250 255
Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser
260 265 270
Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala
275 280 285
Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln
290 295 300
Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro
305 310 315 320
Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro
325 330 335
Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile
340 345 350
Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His
355 360 365
Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr
370 375 380
Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys
385 390 395 400
Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp
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Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg
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<223> Description of Artificial Sequence: primer

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18